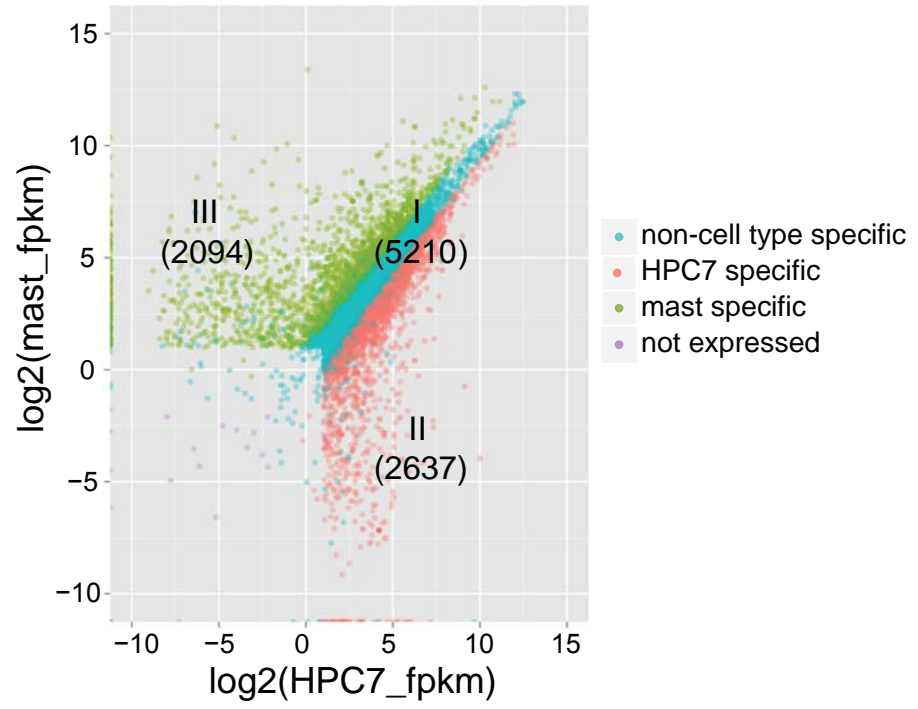
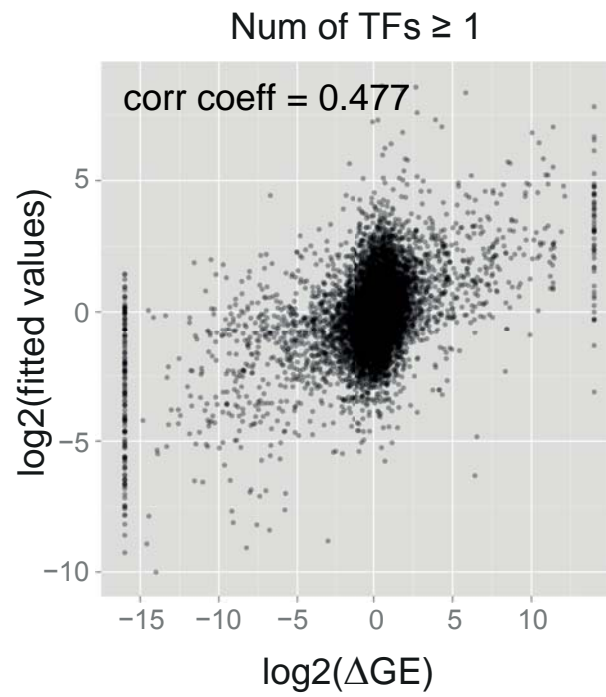


Figure S2

A



B



**Figure S2** – Mathematical modelling of gene expression and transcription factor variability. (A) Scatterplot representing expression (in fpkm values obtained by RNA-seq) for genes bound by at least 1 TF in HPC7 and mast cells used for mathematical modelling. Each dot on the scatterplot is coloured based on 4 categories: (I) non-cell-type specific, (II) HPC7-specific, (III) mast-specific and (IV) not expressed. 58.6% of genes expressed in either cell type are bound by at least 1 shared TF. These genes show similar distribution of expression scores as the entire transcriptome shown in Figure 1. (B) Scatterplot of observed and predicted values from the multiple linear regression model for genes bound by at least 1 shared TF. The range of predicted values for genes with no observed change in expression is very large (predicted  $\Delta GE$  range from -5 to 5 for  $\Delta GE \sim 0$ ).